

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/730,374

DATE: 05/24/2001

TIME: 15:13:14

Input Set : A:\150188us2.txt

Output Set: C:\CRF3\05242001\I730374.raw

ENTERED

5 <110> APPLICANT: Lust, John A.
6 Donovan, Kathleen A.
8 <120> TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES
9 TO CD38 TO TREAT MULTIPLE MYELOMA
12 <130> FILE REFERENCE: 150.188US2
14 <140> CURRENT APPLICATION NUMBER: 09/730,374
C--> 15 <141> CURRENT FILING DATE: 2001-05-10
17 <150> PRIOR APPLICATION NUMBER: PCT/US99/12512
18 <151> PRIOR FILING DATE: 1999-06-04
20 <150> PRIOR APPLICATION NUMBER: 60/088,277
21 <151> PRIOR FILING DATE: 1998-08-05
23 <160> NUMBER OF SEQ ID NOS: 4
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 750
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: A nucleotide sequence encoding a single chain
34 variable region fragment (scFv)
36 <400> SEQUENCE: 1
37 ggcccagccg gccatggcca aggtccagct gcaggagtca ggacctagcc tagtgcagcc 60
38 ctcacagcgc ctgtccataa cctgcacagt ctctggtttc tcattaatta gttatgggtgt 120
39 aacttggtt cgccagctctc caggaaaggg tctggagtgg ctgggagtga tatggagagg 180
40 tggaagcaca gactacaatg cagctttcat gtccagactg agcatcacca aggacaactc 240
41 caagagccaa gttttcttta aaatgaacag tctgcaagct gatgacactg ccatatactt 300
42 ctgtgccaaa accttgatta cgacgggcta tgctatggac tactggggcc aagggaccac 360
43 ggtcaccgtc tcctcaggtg gaggcgggtc aggcggaggt ggctctggcg gtggcggatc 420
44 ggacatcgag ctactcagt ctccatctc cttttctgta tctctaggag acagagtcac 480
45 cattacttgc aaggcaagtg aggacatata taatcgggta gcctgggtatc agcagaaacc 540
46 aggaaatgct cctaggctct taatatctgg tgcaaccagt ttggaaactg gggttccttc 600
47 aagattcagt ggcagtggat ctggaaagga ttacactctc agcattacca gtcttcagac 660
48 tgaagatgtt gctacttatt actgtcaaca gtattggagt actcctacgt tcggtggagg 720
49 gaccaagctg gaaatcaaac gggcgcccg 750
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 241
53 <212> TYPE: PRT
54 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: A polypeptide encoded by an open reading frame of
58 SEQ ID NO:1
60 <400> SEQUENCE: 2
61 Gly Pro Ala Gly His Gly Gln Gly Pro Ala Ala Gly Val Arg Thr Pro
62 1 5 10 15
63 Ser Ala Ala Leu Thr Ala Pro Val His Asn Leu His Ser Leu Trp Phe
64 20 25 30
65 Leu Ile Asn Leu Trp Cys Thr Leu Gly Ser Pro Val Ser Arg Lys Gly

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```

66          35          40          45
67 Ser Gly Val Ala Gly Ser Asp Met Glu Arg Trp Lys His Arg Leu Gln
68          50          55          60
69 Cys Ser Phe His Val Gln Thr Glu His His Gln Gly Gln Leu Gln Glu
70 65          70          75          80
71 Pro Ser Phe Leu Asn Glu Gln Ser Ala Ser His Cys His Ile Leu Leu
72          85          90          95
73 Cys Gln Asn Leu Asp Tyr Asp Gly Leu Cys Tyr Gly Leu Leu Gly Pro
74          100         105         110
75 Arg Asp His Gly His Arg Leu Leu Arg Trp Arg Arg Phe Arg Arg Arg
76          115         120         125
77 Trp Leu Trp Arg Trp Arg Ile Gly His Arg Ala His Ser Val Ser Ile
78          130         135         140
79 Leu Leu Phe Cys Ile Ser Arg Arg Gln Ser His His Tyr Leu Gln Gly
80 145         150         155         160
81 Lys Gly His Ile Ser Val Ser Leu Val Ser Ala Glu Thr Arg Lys Cys
82          165         170         175
83 Ser Ala Leu Asn Ile Trp Cys Asn Gln Phe Gly Asn Trp Gly Ser Phe
84          180         185         190
85 Lys Ile Gln Trp Gln Trp Ile Trp Lys Gly Leu His Ser Gln His Tyr
86          195         200         205
87 Gln Ser Ser Asp Arg Cys Cys Tyr Leu Leu Leu Ser Thr Val Leu Glu
88          210         215         220
89 Tyr Ser Tyr Val Arg Trp Arg Asp Gln Ala Gly Asn Gln Thr Gly Gly
90 225         230         235         240

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91 Arg

94 <210> SEQ ID NO: 3

95 <211> LENGTH: 249

96 <212> TYPE: PRT

97 <213> ORGANISM: Artificial Sequence

99 <220> FEATURE:

100 <223> OTHER INFORMATION: A polypeptide encoded by an open reading frame of

101 SEQ ID NO:1

104 <400> SEQUENCE: 3

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105 Ala Gln Pro Ala Met Ala Lys Val Gln Leu Gln Glu Ser Gly Pro Ser
106 1          5          10          15
107 Leu Val Gln Pro Ser Gln Arg Leu Ser Ile Thr Cys Thr Val Ser Gly
108          20          25          30
109 Phe Ser Leu Ile Ser Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly
110          35          40          45
111 Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Arg Gly Gly Ser Thr Asp
112          50          55          60
113 Tyr Asn Ala Ala Phe Met Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser
114 65          70          75          80
115 Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ala Asp Asp Thr
116          85          90          95
117 Ala Ile Tyr Phe Cys Ala Lys Thr Leu Ile Thr Thr Gly Tyr Ala Met
118          100         105         110
119 Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly

```

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```

120          115          120          125
121 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu
122          130          135          140
123 Thr Gln Ser Pro Ser Ser Phe Ser Val Ser Leu Gly Asp Arg Val Thr
124 145          150          155          160
125 Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg Leu Ala Trp Tyr
126          165          170          175
127 Gln Gln Lys Pro Gly Asn Ala Pro Arg Leu Leu Ile Ser Gly Ala Thr
128          180          185          190
129 Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
130          195          200          205
131 Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr Glu Asp Val Ala
132          210          215          220
133 Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Thr Pro Thr Phe Gly Gly Gly
134 225          230          235          240
135 Thr Lys Leu Glu Ile Lys Arg Ala Ala
136          245
138 <210> SEQ ID NO: 4
139 <211> LENGTH: 239
140 <212> TYPE: PRT
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: A polypeptide encoded by an open reading frame of
145     SEQ ID NO:1
148 <400> SEQUENCE: 4
149 Pro Ser Arg Pro Trp Pro Arg Ser Ser Cys Arg Ser Gln Asp Leu Ala
150 1          5          10          15
151 Cys Ser Pro His Ser Ala Cys Pro Pro Ala Gln Ser Leu Val Ser His
152          20          25          30
153 Leu Val Met Val Tyr Thr Gly Phe Ala Ser Leu Gln Glu Arg Val Trp
154          35          40          45
155 Ser Gly Trp Glu Tyr Gly Glu Val Glu Ala Gln Thr Thr Met Gln Leu
156          50          55          60
157 Ser Cys Pro Asp Ala Ser Pro Arg Thr Thr Pro Arg Ala Lys Phe Ser
158 65          70          75          80
159 Leu Lys Thr Val Cys Lys Leu Met Thr Leu Pro Tyr Thr Ser Val Pro
160          85          90          95
161 Lys Pro Leu Arg Arg Ala Met Leu Trp Thr Thr Gly Ala Lys Gly Pro
162          100          105          110
163 Arg Ser Pro Ser Pro Gln Val Glu Ala Val Gln Ala Glu Val Ala Leu
164          115          120          125
165 Ala Val Ala Asp Arg Thr Ser Ser Ser Leu Ser Leu His Pro Pro Phe
166          130          135          140
167 Leu Tyr Leu Glu Thr Glu Ser Pro Leu Leu Ala Arg Gln Val Arg Thr
168 145          150          155          160
169 Tyr Ile Ile Gly Pro Gly Ile Ser Arg Asn Gln Glu Met Leu Leu Gly
170          165          170          175
171 Ser Tyr Leu Val Gln Pro Val Trp Lys Leu Gly Phe Leu Gln Asp Ser
172          180          185          190

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173	Val	Ala	Val	Asp	Leu	Glu	Arg	Ile	Thr	Leu	Ser	Ala	Leu	Pro	Val	Phe
174			195					200					205			
175	Arg	Leu	Lys	Met	Leu	Leu	Leu	Ile	Thr	Val	Asn	Ser	Ile	Gly	Val	Leu
176		210					215					220				
177	Leu	Arg	Ser	Val	Glu	Gly	Pro	Ser	Trp	Lys	Ser	Asn	Gly	Arg	Pro	
178	225					230						235				

VERIFICATION SUMMARY

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date